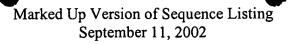SUBSTITUTE SEQUENCE LISTING

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<211> 1791
<212> DNA
<213> Homo sapiens

<400> 3
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```

<400> 4
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Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
 1               5                  10                  15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
             20              25                  30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
         35              40                  45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp
     50                  55                  60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro
 65                  70                  75                  80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val
             85                  90                  95
```

```
Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln
            100             105             110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys
            115             120             125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser
    130             135             140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln
145             150             155             160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg
            165             170             175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Ser Tyr Gln
            180             185             190

Leu Asp Pro Leu Val Thr Pro Val Gly Pro Thr Ser Arg Phe Gly Gly
            195             200             205

Ser Ala His Asn Ile Thr Gln Gly Ile Val Leu Gln Asp Ser Asn Met
210             215             220

Met Ser Leu Lys Ala Leu Ser Phe Ser Asp Gly Gly Ser Lys Leu Gly
225             230             235             240

His Ser Asn Lys Ala Asp Lys Gly Pro Ser Cys Val Arg Ser Pro Ile
            245             250             255

Ser Thr Asp Glu Cys Ser Ile Gln Glu Leu Glu Gln Lys Leu Leu Glu
            260             265             270

Arg Glu Gly Ala Leu Gln Lys Leu Gln Arg Ser Phe Glu Glu Lys Glu
            275             280             285

Leu Ala Ser Ser Leu Ala Tyr Glu Glu Arg Pro Arg Arg Cys Arg Asp
    290             295             300

Glu Leu Glu Gly Pro Glu Pro Lys Gly Gly Asn Lys Leu Lys Gln Ala
305             310             315             320

Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His Leu Gln Val Leu
            325             330             335

Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu
            340             345             350

Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg
            355             360             365

Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val
    370             375             380

Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu
385             390             395             400
```

```
Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys
            405             410             415

Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg
            420             425             430

Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu
            435             440             445

Val Cys Glu Asn Glu Leu Gln Arg Lys Lys Asn Glu Ala Glu Leu Leu
        450             455             460

Arg Glu Lys Val Asn Leu Leu Glu Gln Glu Leu Gln Glu Leu Arg Ala
465                     470             475                 480

Gln Ala Ala Leu Ala Arg Asp Met Gly Pro Pro Thr Phe Pro Glu Asp
                485             490             495

Val Pro Ala Leu Gln Arg Glu Leu Glu Arg Leu Arg Ala Glu Leu Arg
            500             505             510

Glu Glu Arg Gln Gly His Asp Gln Met Ser Ser Gly Phe Gln His Glu
            515             520             525

Arg Leu Val Trp Lys Glu Glu Lys Glu Lys Val Ile Gln Tyr Gln Lys
        530             535             540

Gln Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln Arg Asn Gln Arg Leu
545                 550             555                 560

Glu Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp Ser Ala Gly Glu Pro
                565             570             575

Leu Glu Val Asp Leu Glu Gly Ala Asp Ile Pro Tyr Glu Asp Ile Ile
            580             585             590

Ala Thr Glu Ile
        595


<210> 5
<211> 76
<212> PRT
<213> Homo sapiens

<400> 5
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
1               5               10              15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
            20              25              30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
        35              40              45

Asp Ser Gly His Gly Lys Ala Met Thr Arg Cys Pro Arg Ala Ser Ser
    50              55              60
```

```
Met Ser Gly Ser Cys Gly Arg Arg Arg Arg Arg Arg
65              70              75
```

<210> 6
<211> 69
<212> PRT
<213> Homo sapiens

<400> 6

```
Arg Cys Arg Asp Glu Leu Glu Gly Pro Glu Pro Lys Gly Gly Asn Lys
  1           5               10                  15

Leu Lys Gln Ala Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His
            20              25              30

Leu Gln Val Leu Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu
        35              40              45

Leu Glu Ser Leu Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg
    50              55              60

Ser Tyr Glu Arg Glu
65
```

<210> 7
<211> 68
<212> PRT
<213> Homo sapiens

<400> 7

```
Ile Ser Arg Arg Arg Arg Glu Lys Glu Asn Pro Lys Glu Arg Asn Lys
  1           5               10                  15

Met Ala Ala Ala Lys Cys Arg Asn Arg Arg Arg Glu Leu Thr Asp Thr
            20              25              30

Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu Gln
            35          ,   40              45

Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile
    50              55              60

Leu Ala Ala His
 65
```

<210> 8
<211> 69
<212> PRT
<213> Homo sapiens

<400> 8

```
Ala Trp Glu Arg Glu Leu Ala Glu Leu Arg Gln Gly Cys Ser Gly Lys
```

```
      1                 5                 10                15

      Leu Gln Gln Val Ala Arg Arg Ala Gln Arg Ala Gln Gln Gly Leu Gln
                  20                  25                  30

      Leu Gln Val Leu Arg Leu Gln Gln Asp Lys Lys Gln Leu Gln Glu Glu
                  35                  40                  45

      Ala Ala Arg Leu Met Arg Gln Arg Glu Glu Leu Glu Asp Lys Val Ala
            50                  55                  60

      Ala Cys Gln Lys Glu
       65
                                .
```

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<210> 9
<211> 404
<212> DNA
<213> Homo sapiens

<400> 9
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ctgctgaggt ttggcttctc ccaggactcc ggtcacggca aggccatgac cagatgtcct 180
cgggcttcca gcatgagcgg ctcgtgtgga aggaggagaa ggagaaggtg attcagtacc 240
agaaacagct gcagcagagc tacgtggcca tgtaccagcg gaaccagcgc ctggagaagg 300
ccctgcagca gctggcacgt ggggacagcg ccggggagcc cttggaggtt gacctggaag 360
gggctgacat cccctacgag gacatcatag ccactgagat ctga              404
```

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<210> 10
<211> 633
<212> DNA
<213> Homo sapiens

<400> 10
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ctgctgaggt ttggcttctc ccaggactcc ggtcacggca agtccagctc caaaatgggc 180
aagagcgaag acttcttcta catcaaggtc agccagaaag cccggggctc ccatcaccca 240
gattacacgg cactgtccag cggggattta gggggccagg ctggggtgga ctttgacccg 300
tccacacccc ccaagctcat gcccttctcc aatcagctag aaatgggctc cgagaagggt 360
gcagtgaggc ccacagcctt caagcctgtg ctgccacggt caggagccat cctgcactcc 420
tccccggaga gtgccagcca ccagctgcac cccgcccctc cagacaagcc caaggagcag 480
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agcctgccca cacacagcgc cggggagccc ttggaggttg acctggaagg ggctgacatc 600
ccctacgagg acatcatagc cactgagatc tga                          633
```

```
<210> 11
<211> 1614
<212> DNA
<213> Homo sapiens

<400> 11
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```

```
ctgctgaggt ttggcttctc ccaggactcc ggtcacggca agtccagctc caaaatgggc 180
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<210> 12
<211> 1512
<212> DNA
<213> Homo sapiens

<400> 12
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gccactgaga tc                                                       1512
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<210> 13
<211> 1692
<212> DNA
<213> Homo sapiens

<400> 13
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ctgctgaggt ttggcttctc ccaggactcc ggtcacggca agtccagctc caaaatgggc 180
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<210> 14
<211> 1722
<212> DNA
<213> Homo sapiens

<400> 14
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ctgctgaggt ttggcttctc ccaggactcc ggtcacggca agtccagctc caaaatgggc 180
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gattacacgg cactgtccag cggggattta ggggggccagg ctggggtgga ctttgacccg 300
tccacacccc ccaagctcat gcccttctcc aatcagctag aaatgggctc cgagaagggt 360
gcagtgaggc ccacagcctt caagcctgtg ctgccacggt caggagccat cctgcactcc 420
tccccggaga gtgccagcca ccagctgcac cccgcccctc cagacaagcc caaggagcag 480
gagctgaagc ctggcctgtg ctctggggcg ctgtcagact ccggccggaa ctccatgtcc 540
```

```
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gacagcaaca tgatgagcct gaaggctctg tccttctccg acggaggtag caagctgggc 720
cactcgaaca aggcagacaa gggcccctcg tgtgtccgct cccccatctc cacggacgag 780
tgcagcatcc aggagctgga gcagaagctg ttggagaggg agggcgccct ccagaagctg 840
cagcgcagct ttgaggagaa ggagcttgcc tccagcctgg cctacgagga gcggccgcgg 900
cgctgcaggg acgagctgga gggcccggag cccaaaggcg gcaacaagct caagcaggcc 960
tcgcagaaga gccagcgcgc gcagcaggtc ctgcacctgc aggtactgca gcttcagcag 1020
gagaagcggc agctccggca ggagctcgag agcctcatga aggagcagga cctgctggag 1080
accaagctca ggtcctacga gagggagaag accagcttcg gccccgcgct ggaggagacc 1140
cagtgggagg tgtgccagaa gtcaggcgag atctccctcc tgaagcagca gctgaaggag 1200
tcccagacgg aggtgaacgc caaggctagc gagatcctgg gtctcaaggc acagctgaag 1260
gacacgcggg gcaagctgga gggcctggag ctgaggaccc aggacctgga gggcgccctg 1320
cgcaccaagg gcctggagct ggaggtctgt gagaatgagc tgcagcgcaa gaagaacgag 1380
gcggagctgc tgcgggagaa ggtgaacctg ctggagcagg agctgcagga gctgcgggcc 1440
caggccgccc tggcccgcga catggggccg cccaccttcc ccgaggacgt ccctgccctg 1500
cagcgggagc tggagcggct cgtgtggaag gaggagaagg agaaggtgat tcagtaccag 1560
aaacagctgc agcagagcta cgtggccatg taccagcgga accagcgcct ggagaaggcc 1620
ctgcagcagc tggcacgtgg ggacagcgcc ggggagccct ggaggttga cctggaaggg 1680
gctgacatcc cctacgagga catcatagcc actgagatct ga              1722
```

<210> 15
<211> 76
<212> PRT
<213> Homo sapiens

<400> 15
```
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
 1               5                  10                  15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
            20                  25                  30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
            35                  40                  45

Asp Ser Gly His Gly Lys Ala Met Thr Arg Cys Pro Arg Ala Ser Ser
     50                  55                  60

Met Ser Gly Ser Cys Gly Arg Arg Arg Arg Arg
 65                  70                  75
```

<210> 16
<211> 210
<212> PRT
<213> Homo sapiens

<400> 16
```
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
 1               5                  10                  15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
            20                  25                  30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
```

```
                 35                        40                        45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp
        50                  55                  60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro
65                  70                  75                      80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val
                85                  90                      95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln
            100                 105                 110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys
        115                 120                 125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser
    130                 135                 140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln
145                 150                 155                 160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg
            165                 170                 175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Ala Gly Glu Pro Leu Glu
            180                 185                 190

Val Asp Leu Glu Gly Ala Asp Ile Pro Tyr Glu Asp Ile Ile Ala Thr
        195                 200                 205

Glu Ile
    210


<210> 17
<211> 537
<212> PRT
<213> Homo sapiens

<400> 17
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
    1               5                   10                  15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
                20                  25                  30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
            35                  40                  45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp
        50                  55                  60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro
65                  70                  75                      80
```

```
Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val
            85              90                  95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln
            100             105             110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys
            115             120             125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser
    130             135             140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln
145             150             155                 160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg
            165             170             175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Ser Tyr Gln
            180             185             190

Leu Asp Pro Leu Val Thr Pro Val Gly Pro Thr Ser Arg Phe Gly Gly
        195             200             205

Ser Ala His Asn Ile Thr Gln Gly Ile Val Leu Gln Asp Ser Asn Met
    210             215             220

Met Ser Leu Lys Ala Leu Ser Phe Ser Asp Gly Gly Ser Lys Leu Gly
225             230             235                 240

His Ser Asn Lys Ala Asp Lys Gly Pro Ser Cys Val Arg Ser Pro Ile
            245             250             255

Ser Thr Asp Glu Cys Ser Ile Gln Glu Leu Glu Gln Lys Leu Leu Glu
            260             265             270

Arg Glu Gly Ala Leu Gln Lys Leu Gln Arg Ser Phe Glu Glu Lys Glu
        275             280             285

Leu Ala Ser Ser Leu Ala Tyr Glu Glu Arg Pro Arg Arg Cys Arg Asp
    290             295             300

Glu Leu Glu Gly Pro Glu Pro Lys Gly Gly Asn Lys Leu Lys Gln Ala
305             310             315                 320

Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His Leu Gln Val Leu
            325             330             335

Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu
            340             345             350

Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg
            355             360             365

Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val
    370             375             380
```

```
Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu
385             390             395             400

Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys
                405             410             415

Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg
            420             425             430

Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu
            435             440             445

Val Cys Glu Asn Glu Leu Gln Arg Lys Lys Asn Glu Ala Glu Leu Leu
        450             455             460

Arg Glu Lys His Glu Arg Leu Val Trp Lys Glu Glu Lys Glu Lys Val
465             470             475             480

Ile Gln Tyr Gln Lys Gln Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln
                485             490             495

Arg Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp
            500             505             510

Ser Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly Ala Asp Ile Pro
        515             520             525

Tyr Glu Asp Ile Ile Ala Thr Glu Ile
530             535
```

```
<210> 18
<211> 504
<212> PRT
<213> Homo sapiens

<400> 18
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
  1               5              10                  15


His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
                20              25                  30


Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
            35              40                  45


Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp
        50              55                  60


Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro
65                  70              75                  80


Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val
                85              90                  95


Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln
```

```
                    100                   105                   110

    Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys
            115                   120                   125

    Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser
        130                   135                   140

    Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln
    145                   150                   155                   160

    Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg
                165                   170                   175

    Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Ser Tyr Gln
                180                   185                   190

    Leu Asp Pro Leu Val Thr Pro Val Gly Pro Thr Ser Arg Phe Gly Gly
            195                   200                   205

    Ser Ala His Asn Ile Thr Gln Gly Ile Val Leu Gln Asp Ser Asn Met
        210                   215                   220

    Met Ser Leu Lys Ala Leu Ser Phe Ser Asp Gly Gly Ser Lys Leu Gly
    225                   230                   235                   240

    His Ser Asn Lys Ala Asp Lys Gly Pro Ser Cys Val Arg Ser Pro Ile
                245                   250                   255

    Ser Thr Asp Glu Cys Ser Ile Gln Glu Leu Glu Gln Lys Leu Leu Glu
                260                   265                   270

    Arg Glu Gly Ala Leu Gln Lys Leu Gln Arg Ser Phe Glu Glu Lys Glu
                275                   280                   285

    Leu Ala Ser Ser Leu Ala Tyr Glu Glu Arg Pro Arg Arg Cys Arg Asp
        290                   295                   300

    Glu Leu Glu Gly Pro Glu Pro Lys Gly Gly Asn Lys Leu Lys Gln Ala
    305                   310                   315                   320

    Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His Leu Gln Val Leu
                325                   330                   335

    Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu
                340                   345                   350

    Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg
                355                   360                   365

    Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val
        370                   375                   380

    Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu
    385                   390                   395                   400

    Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys
```

```
                        405                     410                     415

Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg
            420                 425                 430

Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu
            435                 440                 445

Val Cys Glu Asn Glu Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln Arg
        450                 455                 460

Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp Ser
465                 470                 475                 480

Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly Ala Asp Ile Pro Tyr
                485                 490                 495

Glu Asp Ile Ile Ala Thr Glu Ile
            500


<210> 19
<211> 563
<212> PRT
<213> Homo sapiens

<400> 19
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
    1               5                   10                  15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
            20                  25                  30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
            35                  40                  45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp
    50                  55                  60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro
65                  70                  75                  80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val
            85                  90                  95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln
            100                 105                 110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys
            115                 120                 125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser
    130                 135                 140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln
145                 150                 155                 160
```

```
Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg
            165             170             175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Ser Tyr Gln
            180             185             190

Leu Asp Pro Leu Val Thr Pro Val Gly Pro Thr Ser Arg Phe Gly Gly
            195             200             205

Ser Ala His Asn Ile Thr Gln Gly Ile Val Leu Gln Asp Ser Asn Met
    210             215             220

Met Ser Leu Lys Ala Leu Ser Phe Ser Asp Gly Gly Ser Lys Leu Gly
225             230             235             240

His Ser Asn Lys Ala Asp Lys Gly Pro Ser Cys Val Arg Ser Pro Ile
            245             250             255

Ser Thr Asp Glu Cys Ser Ile Gln Glu Leu Glu Gln Lys Leu Leu Glu
            260             265             270

Arg Glu Gly Ala Leu Gln Lys Leu Gln Arg Ser Phe Glu Glu Lys Glu
            275             280             285

Leu Ala Ser Ser Leu Ala Tyr Glu Glu Arg Pro Arg Arg Cys Arg Asp
    290             295             300

Glu Leu Glu Gly Pro Glu Pro Lys Gly Gly Asn Lys Leu Lys Gln Ala
305             310             315             320

Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His Leu Gln Val Leu
            325             330             335

Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu
            340             345             350

Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg
            355             360             365

Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val
    370             375             380

Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu
385             390             395             400

Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys
            405             410             415

Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg
            420             425             430

Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu
            435             440             445

Val Cys Glu Asn Glu Leu Gln Arg Lys Lys Asn Glu Ala Glu Leu Leu
    450             455             460
```

```
Arg Glu Lys Val Asn Leu Leu Glu Arg Leu Arg Ala Glu Leu Arg Glu
465             470             475             480

Glu Arg Gln Gly His Asp Gln Met Ser Ser Gly Phe Gln His Glu Arg
            485             490             495

Leu Val Trp Lys Glu Glu Lys Glu Lys Val Ile Gln Tyr Gln Lys Gln
            500             505             510

Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln Arg Asn Gln Arg Leu Glu
            515             520             525

Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp Ser Ala Gly Glu Pro Leu
    530             535             540

Glu Val Asp Leu Glu Gly Ala Asp Ile Pro Tyr Glu Asp Ile Ile Ala
545             550             555             560

Thr Glu Ile
```

<210> 20
<211> 573
<212> PRT
<213> Homo sapiens

<400> 20
```
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
  1             5               10              15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
            20              25              30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
            35              40              45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp
    50              55              60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro
65              70              75              80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val
            85              90              95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln
            100             105             110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys
            115             120             125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser
    130             135             140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln
```

```
        145                    150                    155                    160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg
            165                    170                    175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Ser Tyr Gln
            180                    185                    190

Leu Asp Pro Leu Val Thr Pro Val Gly Pro Thr Ser Arg Phe Gly Gly
            195                    200                    205

Ser Ala His Asn Ile Thr Gln Gly Ile Val Leu Gln Asp Ser Asn Met
            210                    215                    220

Met Ser Leu Lys Ala Leu Ser Phe Ser Asp Gly Gly Ser Lys Leu Gly
225                    230                    235                    240

His Ser Asn Lys Ala Asp Lys Gly Pro Ser Cys Val Arg Ser Pro Ile
            245                    250                    255

Ser Thr Asp Glu Cys Ser Ile Gln Glu Leu Glu Gln Lys Leu Leu Glu
            260                    265                    270

Arg Glu Gly Ala Leu Gln Lys Leu Gln Arg Ser Phe Glu Glu Lys Glu
            275                    280                    285

Leu Ala Ser Ser Leu Ala Tyr Glu Glu Arg Pro Arg Arg Cys Arg Asp
            290                    295                    300

Glu Leu Glu Gly Pro Glu Pro Lys Gly Gly Asn Lys Leu Lys Gln Ala
305                    310                    315                    320

Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His Leu Gln Val Leu
            325                    330                    335

Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu
            340                    345                    350

Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg
            355                    360                    365

Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val
            370                    375                    380

Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu
385                    390                    395                    400

Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys
            405                    410                    415

Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg
            420                    425                    430

Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu
            435                    440                    445

Val Cys Glu Asn Glu Leu Gln Arg Lys Lys Asn Glu Ala Glu Leu Leu
```

```
         450              455              460

Arg Glu Lys Val Asn Leu Leu Glu Gln Glu Leu Gln Glu Leu Arg Ala
465             470              475              480

Gln Ala Ala Leu Ala Arg Asp Met Gly Pro Pro Thr Phe Pro Glu Asp
            485              490              495

Val Pro Ala Leu Gln Arg Glu Leu Glu Arg Leu Val Trp Lys Glu Glu
        500              505              510

Lys Glu Lys Val Ile Gln Tyr Gln Lys Gln Leu Gln Gln Ser Tyr Val
        515              520              525

Ala Met Tyr Gln Arg Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu
    530              535              540

Ala Arg Gly Asp Ser Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly
545             550              555              560

Ala Asp Ile Pro Tyr Glu Asp Ile Ile Ala Thr Glu Ile
            565              570
```

```
<210> 21
<211> 591
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: F37 Probe

<400> 21
ggactctgcc cctggacctg ggaacgactg gactgtcacg gggttccctc ctagctctcc 60
cagtgaactc ctgccaggca cacacagccc ctatagcact gagctcacat gggactggga 120
tatgggggca tctcttcccc agagaggcac tcagtgagcc tcctgtgcct ggccccagtc 180
tgggccatct cttaggtgag acagttgccc gaaactaagc caggcctggc tggaggagca 240
gcagcttggg gagagggatt tccctgcaga cctcaagcca tcatgcggtg ggtgctgcca 300
tgacagaggc tgcacccctg ggccagcggg gctgctcacc cacctcttgt gcaaggtggc 360
ctttgtgctg cgcctgcagg cagagctgga gcccccagca gaggcaggct gggacggacc 420
agcatctgga agatgtacat agttatttttt ctctttgtgg tttcttgttt ggtttggttt 480
gcttttgaca gcttcatttt atttttgacg tcacttttttg gccatgtaaa ctatttgtgg 540
caattttatg tttttatttta tgaataaaga atgccatttc tcacgccctc t          591
```

```
<210> 22
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
      region amplificatin primer G12

<400> 22
gctgccacag cctttccaag acc
```

23

```
<210> 23
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
      region amplificatin primer G13

<400> 23
taccggttga gcttcttgag gtg                                          23


<210> 24
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
      region amplification primer G14.2

<400> 24
acagcttcca cagcaagcac tgc                                          23


<210> 25
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
      region amplification primer G15

<400> 25
attggagaag ggcatgagct t                                            21


<210> 26
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
      region amplification primer G16

<400> 26
tggactttga cccgtccaca cc                                           22


<210> 27
<211> 23
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
     region amplification primer IntABR

<400> 27
gtttccaacc cacttaccct tgc   23

<210> 28
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
     region amplification primer IntABF

<400> 28
gcaggggagg catgagtcac c   21

<210> 29
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
     region amplification primer G17

<400> 29
ggcttcagct cctgctcctt gg   22

<210> 30
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
     region amplification primer G20

<400> 30
acaacatcac ccagggcatc gtc   23

<210> 31
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
     region amplification primer G21

```
<400> 31
cctccagctc gtccctgcag c                                          21


<210> 32
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
      region amplification primer G32

<400> 32
actgcagctt cagcaggaga agc                                        23


<210> 33
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
      region amplification primer IntBCR

<400> 33
ctgaccaccc aaacccatga gc                                         22


<210> 34
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
      region amplification primer IntBCF

<400> 34
tcacctcttg gcactctgtc tcc                                        23


<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
      region amplification primer Mut6

<400> 35
caggtcctgg gtcctcagct c                                          21


<210> 36
```

```
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
      region amplification primer G1

<400> 36
tgaacgccaa ggctagcgag atc                                              23


<210> 37
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
      region amplification primer G2

<400> 37
gctcctgcag ctcctgctcc ag                                               22


<210> 38
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
      region amplification primer G75

<400> 38
cccaccttcc ccgaggacgt c                                                21


<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
      region amplification primer G82

<400> 39
agcccgagga catctggtca tgg                                              23


<210> 40
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
```

<223> Description of Artificial Sequence: FEZ1 alterable
    region amplification primer G5

<400> 40
cctgccctgc agcgggagct ggag   24

<210> 41
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
    region amplification primer G6

<400> 41
agctgctgca gggccttctc cag   23

<210> 42
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
    region amplification primer G7

<400> 42
cagtaccaga aacagctgca gcagagc   27

<210> 43
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FEZ1 alterable
    region amplification primer G8

<400> 43
ccctgcctcc cagtgccagg tc   22

<210> 44
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: First strand
    of partially-double stranded adapter-linker

<400> 44
gatctcgacg aattcgtgag acct   24

<210> 45
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Second strand
      of partially-double stranded adapter-linker

<400> 45
tggtctcacg aattcgtcga   20

<210> 46
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Donor site
      sequence of truncated FEZ1 truncation region

<400> 46
tcccaggact ccggtcacgg caa   23

<210> 47
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acceptor site
      sequence of truncated FEZ1 truncation region

<400> 47
gagcggcaag gccatgacca g   21

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Donor site
      sequence of truncated FEZ1 truncation region

<400> 48
agcctgccca cacacagcac cag   23

<210> 49
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 49
cagcgccggg gagcccttgg a   21

<210> 50
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Donor site
sequence of truncated FEZ1 truncation region

<400> 50
gtgagaatga gctgcagcgc aag   23

<210> 51
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 51
cagcagagct acgtggccat gt   22

<210> 52
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Donor site
sequence of truncated FEZ1 truncation region

<400> 52
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<210> 53
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

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<210> 54
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<220>
<223> Description of Artificial Sequence: Donor  site
      sequence of truncated FEZ1 truncation region

<400> 54
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<210> 55
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acceptor site
      sequence of truncated FEZ1 truncation region

<400> 55
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<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Donor site
      sequence of truncated FEZ1 truncation region

<400> 56
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<210> 57
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acceptor site
      sequence of truncated FEZ1 truncation region

<400> 57
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<210> 58
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer for
      amplifying FEZ1 cDNA

<400> 58
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<210> 59
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer for
      amplifying FEZ1 cDNA

<400> 59
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<210> 60
<211> 8073
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nucleotide
      sequence of vector pQBI-AdCMV5-IRES-GFP

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<212> DNA
<213> Artificial Sequence


<220>
<223> Description of Artificial Sequence: Example

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<210> 62
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<220>
<223> Description of Artificial Sequence: Example

<400> 62
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<210> 63
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<220>
<223> Description of Artificial Sequence: Example


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aaccaaaaaa c                                                      11



<210> 64
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<220>
<223> Description of Artificial Sequence: Example

<400> 64
aaccaaaaaa g                                                      11


<210> 65
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gcgcaagtcc ccccacctca agaa                                     24


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<210> 69
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<210> 70
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